WHAT IS CLAIMED IS:

1. A crystallized mammalian fatty acid amide hydrolase (FAAH).

2. The crystallized FAAH of claim 1, wherein said enzyme has an amino acid sequence of SEQ. ID. NO.1, or conservative substitutions thereof.

3. A three-dimensional model for the structure of FAAH at the secondary, tertiary, and quaternary levels.

4. A method for determining the three-dimensional structure of FAAH from the crystals of claim 1, comprising collecting X-ray diffraction data from said crystal, and analyzing said data by multiple isomorphous replacement (MIR) and single-and multiwavelength anomalous diffraction (SAD/MAD), thereby determining the three-dimensional structure of FAAH.

5. A method for determining the molecular structure of a molecule or molecular complex whose structure is unknown, comprising

(a) obtaining crystals of the molecule or molecular complex whose structure is unknown;

(b) generating X-ray diffraction data from the crystallized molecule or molecular complex;

(c) comparing the X-ray diffraction data from the molecule or molecular complex with the three dimensional structure determined from the crystal of claim 1; and

(d) using molecular replacement analysis to conform the three dimensional structure determined from the crystal of claim 1 to the X-ray diffraction data from the crystallized molecule or molecular complex.

6. A method for identifying an agent that interacts with an internal channel of FAAH, comprising performing manual or computer assisted fitting analysis of the agent with the three-dimensional model of claim 3, thereby identifying an agent that interacts with an internal channel of FAAH.

7. The method of claim 6, wherein the internal channel is the active site.

8. The method of claim 7, wherein the active site comprises amino acid residues 142, 217, 218, 236, 238, 239, 240 and 241.

9. The method of claim 6, wherein the internal channel is the substrate binding pocket.

10. The method of claim 9, wherein the substrate binding pocket comprises amino acid residues 491, 495, 335, 372, 377, 194, and 244.

11. The method of claim 9, wherein the interaction of the agent with the substrate binding pocket is identified, optimized, or compared to the position of arachidonyl inhibitor MAFP.

12. The method of claim 6, wherein the internal channel is the membrane port of FAAH.

13. The method of claim 12, wherein the membrane port comprises amino acid residues 403, 407, 428, 429, 486, 530, and 534.

14. The method of claim 6, wherein the internal channel is the cytosolic port of FAAH.

15. The method of claim 14, wherein the cytosolic port comprises amino acid residues 266, 271,272, 445, 449, and 453.

16. The method of claim 6, wherein the internal channel is the dimerization tunnel of FAAH.

17. The method of claim 16, wherein the dimerization tunnel comprises amino acid residues 257, 259, 261, 262, 263, 264, 306, 308, 309, 448, 451, 452, 455, 456, 499, 500, 501, and 556.

18. The method of claim 6, wherein the internal channel is the membrane-binding domain of FAAH.

19. The method of claim 18, wherein the membrane-binding domain comprises amino acid residues 383-440.

20. The method of claim 6, wherein the internal channel is the head group tunnel of FAAH.

21. The method of claim 20, wherein the head group tunnel comprises amino acid residues 268, 269, 270, 273, 274, 275, 276, 277, and 278.

22. The method of claim 6, wherein the internal channel is the alkyl tunnel of FAAH.

23. The method of claim 22, wherein the alkyl tunnel comprises amino acid residues 190-194, 244, 335, 372, 373, 376, 377, 380, 381, 388, 401, 402, 404, 432, 484, 485, 488, 489, 491, 492, 495, and 531.

24. A method for identifying an agent that interacts with the SH3-binding domain of FAAH, comprising performing manual or computer assisted fitting analysis of the agent with the three-dimensional model of claim 3, thereby identifying an agent that interacts with the SH3-binding domain of FAAH.

25. The method of claim 24, wherein the SH3-binding domain comprises amino acid residues 297-315.

26. A method for identifying an agent that interacts with the surface helix-loop-helix of FAAH, comprising performing manual or computer assisted fitting analysis of the agent with the three-dimensional model of claim 3, thereby identifying an agent that interacts with the surface helix-loop-helix of FAAH.

27. The method of claim 26, wherein the surface helix-loop-helix comprises amino acid residues 511-546.

28. An agent identified by the methods of any one of claims 6 - 27.

29. A pharmaceutical composition comprising an agent of claim 28 and a pharmaceutically acceptable carrier therefor.

30. A method for treating a pathological condition, comprising administering to a subject in need thereof a pharmaceutical composition according to claim 29, thereby treating the pathological condition.

31. The method of claim 30, wherein said subject is a mammal.

32. The method of claim 31, wherein said mammal is human.

33. The method of claim 30, wherein said pathological condition is anxiety, pain, hunger, sleep, fertility, cognition, immunological disorders, fever, tremor, glaucoma, or intestinal disorders.

34. A method for screening an agent for the ability to modulate the activity of FAAH, comprising contacting FAAH with the agent to form a FAAH-agent complex, and measuring the activity level of said FAAH-agent complex relative to un-complexed FAAH, thereby screening the agent for the ability to modulate the activity of FAAH

35. A method for evaluating the effects of agents identified by claim 34, comprising administering the agents to living cells or a living organism.

36. A method for engineering FAAH variants with altered substrate specificities or kinetics, comprising identifying the substrate binding site of FAAH, and altering said substrate binding site, thereby engineering FAAH variants with altered substrate specificities or kinetics.

37. A method for altering membrane tropism of a heterologous protein, comprising transplanting the entire membrane binding domain of FAAH to the heterologous protein, thereby altering membrane tropism of a heterologous protein.

38. A method for altering membrane tropism of a heterologous protein, comprising transplanting a portion of the membrane binding domain of FAAH to the heterologous protein, thereby altering membrane tropism of a heterologous protein.

39. A method for engineering FAAH variants with altered membrane-binding properties, comprising identifying the membrane-binding domain of FAAH, and altering said membrane-binding domain, thereby engineering FAAH variants with altered membrane-binding properties.